1

Amended Claims

1. A method for estimating the skin cancer, lung cancer, breast cancer and colon
   cancer risk of an individual comprising

   - assessing in the genetic material of a sample from said individual a sequence
     polymorphism

     - in a region corresponding to SEQ ID NO: 2, or a part thereof, or
     - in a region complementary to SEQ ID NO: 2, or a part thereof, or
     - in a transcription product from a sequence in a region corresponding to SEQ
       ID NO: 2, or a part thereof, or
     - or translation product from a sequence in a region corresponding to SEQ ID
       NO: 2, or a part thereof,
     - obtaining a sequence polymorphism response,

   - estimating the skin cancer, lung cancer, breast cancer and colon cancer risk of
     said individual based on the sequence polymorphism response.

2. The method according to claim 1, wherein a sequence polymorphism is as-
   sessed

   - in a region corresponding to SEQ ID NO: 1, or a part thereof, or
   - in a region complementary to SEQ ID NO: 1, or a part thereof, or
   - in a transcription product from a sequence in a region corresponding to SEQ ID
     NO: 1, or a part thereof, or
   - or translation product from a sequence in a region corresponding to SEQ ID
     NO: 1, or a part thereof.

3. The method according to claim 1, wherein the cell sample is a blood sample, a
   tissue sample, a sample of secretion, semen, ovum, a washing of a body sur-
   face, such as a buccal swap, a clipping of a body surface, including hairs and
   nails.

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4. The method according to any of the preceding claims, wherein the cell is selected from white blood cells and tumor tissue.

5 5. The method according to any of the preceding claims, wherein the sequence polymorphism comprises at least one mutation base change.

6. The method according to any of the preceding claims, wherein the sequence polymorphism comprises at least two base changes.

10

7. The method according to any of the preceding claims, wherein the sequence polymorphism comprises at least one single nucleotide polymorphism.

8. The method according to any of the preceding claims, wherein the sequence
15 polymorphism comprises at least two single nucleotide polymorphisms.

9. The method according to any of the preceding claims, wherein the sequence polymorphism comprises at least one tandem repeat polymorphism.

20 10. The method according to any of the preceding claims, wherein the sequence polymorphism comprises at least two tandem repeat polymorphisms.

11. The method according to any of the preceding claims, wherein the assessment is conducted by means of at least one nucleic acid primer or probe, such as a
25 primer or probe of DNA, RNA or a nucleic acid analogue such as peptide nucleic acid (PNA) or locked nucleic acid (LNA).

12. The method according to claim 11, wherein the nucleotide primer or probe is capable of hybridising to a subsequence of the region corresponding to SEQ ID
30 NO: 1, or a part thereof, or a region complementary to SEQ ID NO:1.

13. The method according to claim 11, wherein the primer or probe has a length of at least 9 nucleotide or peptide monomers.

3

14. The method according to any of the preceding claims 11-13, wherein at least
    one primer or probe is capable of hybridising to a subsequence selected from
    the group of subsequences

5
1. GCTCTGAAAC TTACTAGCCC(A/G)GTATTTATGG AGAGGCATTT

2. GTGGTCAAAT TCTCATTCAT CGTGG (T/C) CCAGGCAAGC
   ACACTTCCTC

3. ACCCTGAGGT GAGCACCTGT TCCTT(C/T) TCCTTGCCCT TAGCCCA-
   GAG GTAGA

10
4. GGGCAGGGGT TTGTGCCTCC AATGA (G/A) CACAAGCTCC
   CCCTGCCCCC CAACT

5. CCTGGCGGTG GCCGTCACCA GCTTT (T/C) GGGGGTGTTT
   GGGAAGCTGG

6. CTCCAGCCCC ACTGTTCCCT (A/G) GGCCCTATTG GTCCCCCTGG

15
7. ACAAGGAGGA GGCAGAAGTG AGGTT (G/C) AAACCCACTG CCCAATC-
   TTA

8. CCAACACGGT GAAACCCCGT CTGTA(T/C)TAAAAATACA AAAATTAGCC

9. AATCCAGGAC CCCATAATCT TCCGT (C/T) ATCTAAAACA ATA-
   ATGGTGA

20
10. CCCAAGGGGG CGAGGGGAGG GTGAA (A/G)GGGTGGGACG
    GGGGCAGCCG

11. GAAGTGAGAA GGGGGCTGGG GGTCG (G/-) CGCTCGCTAG
    CGGGCGCGGG

12. CGCACGCGCA GTATCCCGAT TGGCT (C/G)TGCCCTAGCG GATT-

25
    GACGGG

13. AACTCCTGGG TTCGATCAAT ACTCA (GACA/-) ATCTTGGCAG
    GCGCAGGAGG

14. GCTGGGATTA CAGGCTTGAG CCACC (A/G) CGCCCGGCCT
    GCAAAGCCAT

30
15. TTTTGTATCT TTAGTAGAGA CAGG (T/G) TTTCTCCATG TTGGTCAGGC

16. GCCTCAGCCT CCCGAGTAGC TGAGACT (C/A) CAGGTGCCCG CCAC-
    CACGCC

17. TGAAATTGTA GGTTGAGAGG CCAGGCG (C/T) GGTGCTCACG
    CCTGTAATTT

35
18. GTTTATAAAC ATTAAACCAG (T/A) GCTGTGTGAA GGCACTTAAT

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19. CCGTCTCTAT TAAAAATATA AAA (A/C) AATTTAGCCG GGTGTAGCGG

20. GGGAGGCTCG AGGCGGGC (A/G) GATTGCATGA GCTCAGGATT

21. TCCCAAGTTT CAGGGCCCAA (T/G) ATTCTCAAAT CACAGGATTC

22. TGCAGTGAGC TGAGATCGC (A/G) CCACTGCACT CCAGCCTGGG

23. TCTTAGGACG CATGGGGGT (T/G) GAGAGAACGG GGAGATAGAC

24. CTGGGTTCTA GAACTACC (C/T) ATGCAAACCC AGCTGTTTCC

25. ATTCTGCCCT GGGTTCTAGA ACTACCT (C/A) TGCAAACCCA
    GCTGTTTCCC

26. GCTGTTTCCC ACCCCATAAG GCA (A/G) TAGGGGAGCC
    CACCTCCGCC

27. GACCTAGAAG ATCGGTCGAG A (C/T) AGCAGCTTGA GGCTGGCAGG

28. CTGGCCAGGA ATGCAGTCGG GTCAC (C/T) CTGTCTAGCC
    ACCGTCTCGC

29. GGGAGGAGTC GCCGATCAGG (C/T) CCCTTCCTGA AAGTCATCGA

30. GCAGCCCGGG CTACAGGGTT (A/G) CCTGAGGTGT GGGTCCCAGG

31. TAGAAATACT AACAAAGGGC (T/C) GTGGGTTTCT CCCCCTGCTT

32. ACAGGAGAGG GAAGGTTTTTTG (A/T) TTTTTTTTTT GTTTTTTTTT

33. GAAGAGGAAG AAGCCCAAAG GGA (A/C) AGAAACCTTC GAGCCA-
    GAAG

34. GCGCCTCAAC AGCCAGAAGG AGCG (A/G) AGCCTCAGGC CCAGG-
    CAGCT

35. TTGAGACTCT CTGTTTGAT (A/G) CTTCACTCAG AAGGTGCTTC

36. AGGCCAGGCT CCTGCTGGCT G (C/G) GCTGGTGCAG TCTCTGGGGA

37. CCCCTATACC CTCAAGCAT (C/T) TATCCATTGA GTTACAAACA

38. ACCATCCCCC GCCTTCCGTT (A/C) GTCCGGCCCC CGAGGCTAGC

or to a sequence complementary to any of the subsequences.

15. The method according to claim 14, wherein at least one nucleotide probe is se-
lected from the group consisting of

1. TGAAATTGTA GGTTGAGAGG CCAGGCG (C/T) GGTGCTCACG
   CCTGTAATTT

2. GTTTATAAAC ATTAAACCAG (T/A) GCTGTGTGAA GGCACTTAAT

3. CCGTCTCTAT TAAAAATATA AAA (A/C) AATTTAGCCG GGTGTAGCGG

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4. GGGAGGCTCG AGGCGGGC (A/G) GATTGCATGA GCTCAGGATT

5. TCCCAAGTTT CAGGGCCCAA (T/G) ATTCTCAAAT CACAGGATTC

6. TGCAGTGAGC TGAGATCGC (A/G) CCACTGCACT CCAGCCTGGG

7. TCTTAGGACG CATGGGGGT (T/G) GAGAGAACGG GGAGATAGAC

8. CTGGGTTCTA GAACTACC (C/T) ATGCAAACCC AGCTGTTTCC

9. ATTCTGCCCT GGGTTCTAGA ACTACCT (C/A) TGCAAACCCA
GCTGTTTCCC

10. GCTGTTTCCC ACCCCATAAG GCA (A/G) TAGGGGAGCC
CACCTCCGCC

11. GACCTAGAAG ATCGGTCGAG A (C/T) AGCAGCTTGA GGCTGGCAGG

12. CTGGCCAGGA ATGCAGTCGG GTCAC (C/T) CTGTCTAGCC
ACCGTCTCGC

13. GGGAGGAGTC GCCGATCAGG (C/T) CCCTTCCTGA AAGTCATCGA

14. GCAGCCCGGG CTACAGGGTT (A/G) CCTGAGGTGT GGGTCCCAGG

15. TAGAAATACT AACAAAGGGC (T/C) GTGGGTTTCT CCCCCTGCTT

16. ACAGGAGAGG GAAGGTTTTTTG (A/T) TTTTTTTTTT GTTTTTTTTT

17. GAAGAGGAAG AAGCCCAAAG GGA (A/C) AGAAACCTTC GAGCCA-
GAAG

18. GCGCCTCAAC AGCCAGAAGG AGCG (A/G) AGCCTCAGGC CCAGG-
CAGCT

or to a sequence complementary to any of the subsequences.

16. The method according to claim 15, wherein at least one nucleotide probe is se-
lected from the group consisting of

1. GTTTATAAAC ATTAAACCAG (T/A) GCTGTGTGAA GGCACTTAAT

2. CCGTCTCTAT TAAAAATATA AAA (A/C) AATTTAGCCG GGTGTAGCGG

3. GGGAGGCTCG AGGCGGGC (A/G) GATTGCATGA GCTCAGGATT

4. TCCCAAGTTT CAGGGCCCAA (T/G) ATTCTCAAAT CACAGGATTC

5. TGCAGTGAGC TGAGATCGC (A/G) CCACTGCACT CCAGCCTGGG

or to a sequence complementary to any of the subsequences.

6

17. The method according to any of the preceding claims, wherein at least one sequence polymorphism is assessed in a region corresponding to SEQ ID NO: 1 position 1521-37752 (r).

5   18. The method according to any of the preceding claims, wherein at least one sequence polymorphism is assessed in a region corresponding to SEQ ID NO: 1 position 7760-22885 (RAI).

       19. The method according to any of the preceding claims, wherein at least one sequence polymorphism is assessed in a region corresponding to SEQ ID NO: 1
10   position 34391- 37752.

       20. The method according to any of the preceding claims, wherein at least two different probes are used, one probe being selected from the probes as defined in
15   any of claims 13-16, and the other probe being capable of hybridising to a sequence different from SEQ ID NO: 1, or a part thereof, or to a sequence complementary to a region different from SEQ ID NO: 1, or a part thereof,.

       21. The method according to claim 1, wherein the translational product from a sequence
20   quence in a region corresponding to SEQ ID NO: 1, or a part thereof, is an antibody, such as a monoclonal or polyclonal antibody.

       22. A method for estimating the disease prognosis of an individual comprising

25

       - assessing in the genetic material of a sample from said individual a sequence polymorphism

       - in a region corresponding to SEQ ID NO: 2, or a part thereof, or
30   - in a region complementary to SEQ ID NO: 2, or a part thereof, or
       - in a transcription product from a sequence in a region corresponding to SEQ ID NO: 2, or a part thereof, or
       - or translation product from a sequence in a region corresponding to SEQ ID NO: 2, or a part thereof,
35   - obtaining a sequence polymorphism response,

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7.

- estimating the disease prognosis of said individual based on the sequence
polymorphism response.

5   23. The method according to claim 22, wherein the method has any of the features
as defined in any of the claims 2-21.

24. A method for estimating a treatment response of an individual suffering from
cancer to a disease treatment, comprising

10

- assessing in the genetic material of a sample from said individual a sequence
polymorphism

- in a region corresponding to SEQ ID NO: 1, or a part thereof, or
15   - in a region complementary to SEQ ID NO: 1, or a part thereof, or
- in a transcription product from a sequence in a region corresponding to
SEQ ID NO: 1, or a part thereof, or
- or translation product from a sequence in a region corresponding to SEQ ID
NO: 1, or a part thereof.

20   - obtaining a sequence polymorphism response,

- estimating the individual's response to the disease treatment based on the
sequence polymorphism response.

25   25. The method according to claim 24, wherein the method has any of the features
as defined in any of the claims 2-21.

26. A primer or probe for detecting polymorphisms for use in a method as defined in
any of the claims above, said primer or probe being selected from

30

TGGCTAACACGGTGAAACC(SEQ ID NO:7)
GGAATCCAAAGATTCTATGATGG(SEQ ID NO:8)
GGGAGGCGGAGCTTGCAGTGA (SEQ ID NO:9)
CTGAGATCGCACCACTGCAC (SEQ ID NO:10)
35   GGTTTTCTGCTCTGCACACG (SEQ ID NO:11)

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CCTTTCTCCTTCCACCAACG (SEQ ID NO:12)

CGGGCTACAGGGTTACCTGAG (SEQ ID NO:13)

TCTGCAACCTGGTGCGAGCAGC (SEQ ID NO:14)

CCTACCACCATCATCACATCC (SEQ ID NO:15)

5   GCCTTGCCAAAAATCATAACC (SEQ ID NO:16)

CCTCTCCCCAATTAAGTGCCTTCACACAGC (SEQ ID NO:17)

AGCCAGGGAGGTTGAGGCT (SEQ ID NO:18)

AGACAGCCCTGAATCAGCAC (SEQ ID NO:19)

GCAATGAGCCGAGATAGAA (SEQ ID NO:20)

10   TGGCTAGCCCATTACTCTA (SEQ ID NO:21)

27. The primer or probe according to claim 26, wherein the probe is operably linked
to at least one label, such as operably linked to two different labels.

15   28. The probe according to claim 27, wherein the label is selected from TEX, TET,
TAM, ROX, R6G, ORG, HEX, FLU, FAM, DABSYL, Cy7, Cy5, Cy3, BOFL, BOF,
BO-X, BO-TRX, BO-TMR, JOE, 6JOE, VIC, 6FAM, LCRed640, LCRed705,
TAMRA, Biotin, Digoxigenin, DuO-family, Daq-family.

20   29. The primer or probe according to any of claims 26-28, wherein the primer or
probe is operably linked to a surface.

30. The primer or probe according to claim 29, wherein the surface is the surface of
microbeads or a DNA chip.

25

31. A kit for use in a method as defined in any of the claims above, comprising at
least one primer or probe, said probe being as defined in any of claims 26-30,
and optionally further amplifying means for nucleic acid amplification.

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